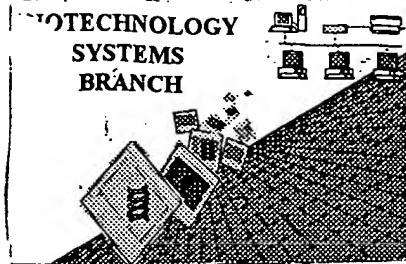


O/PE

RECEIVED

MAR 21 2002



1664

CRF Problem Report

TECH CENTER 1600/2900

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 09/634,287

Filing Date: 8/9/2000

Date Processed by STIC: 3/4/2002

STIC Contact: Mark Spencer, 703-308-4212

Nature of Problem:

The CRF (was):

- Damaged or Unreadable (for Unreadable, see attached)
 Blank (no files on CRF) (see attached)
 Empty file (filename present, but no bytes in file) (see attached)
 Virus-infected. Virus name: _____ The STIC will not process the CRF.
 Not saved in ASCII text
 Sequence Listing was embedded in the file. According to Sequence Rules,
submitted file should only be the Sequence Listing.
 Did not contain a Sequence Listing. (see attached sample)
 Other:

PLEASE USE THE CHECKER VERSION 3.1 PROGRAM TO REDUCE ERRORS.

SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service , or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

BEST AVAILABLE COPY

ADMP-1 Sequences

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 4192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 406..2919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACA GAC ACA TAT GCA CGA GAG AGA CAG AGG AGG AAA GAG ACA GAG ACA	48
AAG GCA CAG CGG AAG AAG GCA GAG ACA GGG CAG GCA CAG AAG CGG CCC	96
AGA CAG AGT CCT ACA GAG GGA GAG GCC AGA GAA GCT GCA GAA GAC ACA	144
GGC AGG GAG AGA CAA AGA TCC AGG AAA GGA GGG CTC AGG AGG AGA GTT	192
TGG AGA AGC CAG ACC CCT GGG CAC CTC TCC CAA GCC CAA GGA CTA AGT	240
TTT CTC CAT TTC CTT TAA CGG TCC TCA GCC CTT CTG AAA ACT TTG CCT	288
CTG ACC TTG GCA GGA GTC CAA GCC CCC AGG CTA CAG AGA GGA GCT TTC	336
CAA AGC TAG GGT GTG GAG GAC TTG GTG CCC TAG ACG GCC TCA GTC CCT	384
CCC AGC TGC AGT ACC AGT GCC ATG TCC CAG ACA GGC TCG CAT CCC GGG Met Ser Gln Thr Gly Ser His Pro Gly	432
AGG GGC TTG GCA GGG CGC TGG CTG TGG GGA GCC CAA CCC TGC CTC CTG Arg Gly Leu Ala Gly Arg Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu	480
CTC CCC ATT GTG CCG CTC TCC TGG CTG GTG TGG CTG CTT CTG CTA CTG Leu Pro Ile Val Pro Leu Ser Trp Leu Val Trp Leu Leu Leu Leu	528
CTG GCC TCT CTC CTG CCC TCA GCC CGG CTG GCC AGC CCC CTC CCC CGG Leu Ala Ser Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg	576
GAG GAG GAG ATC GTG TTT CCA GAG AAG CTC AAC GGC AGC GTC CTG CCT Glu Glu Glu Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro	624
GGC TCG GGC GCC CCT GCC AGG CTG TTG TGC CGC TTG CAG GCC TTT GGG Gly Ser Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly	672
GAG ACG CTG CTA CTA GAG CTG GAG CAG GAC TCC GGT GTG CAG GTC GAG Glu Thr Leu Leu Leu Glu Leu Gln Asp Ser Gly Val Gln Val Glu	720
GGG CTG ACA GTG CAG TAC CTG GGC CAG GCG CCT GAG CTG CTG GGT GGA Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly Gly	768
GCA GAG CCT GGC ACC TAC CTG ACT GGC ACC ATC AAT GGA GAT CCG GAG Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp Pro Glu	816

TCG GTG GCA TCT CTG CAC TGG GAT GGG GGA GCC CTG TTA GGC GTG TTA	864
Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu Gly Val Leu	
CAA TAT CGG GGG GCT GAA CTC CAC CTC CAG CCC CTG GAG GGA GGC ACC	912
Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro Leu Glu Gly Gly Thr	
CCT AAC TCT GCT GGG GGA CCT GGG GCT CAC ATC CTA CGC CGG AAG AGT	960
Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile Leu Arg Arg Lys Ser	
CCT GCC AGC GGT CAA GGT CCC ATG TGC AAC GTC AAG GCT CCT CTT GGA	1008
Pro Ala Ser Gly Gln Gly Pro Met Cys Asn Val Lys Ala Pro Leu Gly	
AGC CCC AGC CCC AGA CCC CGA AGA GCC AAG CGC TTT GCT TCA CTG AGT	1056
Ser Pro Ser Pro Arg Pro Arg Ala Lys Arg Phe Ala Ser Leu Ser	
AGA TTT GTG GAG ACA CTG GTG GCA GAT GAC AAG ATG GCC GCA TTC	1104
Arg Phe Val Glu Thr Leu Val Val Ala Asp Asp Lys Met Ala Ala Phe	
CAC GGT GCG GGG CTA AAG CGC TAC CTG CTA ACA GTG ATG GCA GCA GCA	1152
His Gly Ala Gly Leu Lys Arg Tyr Leu Leu Thr Val Met Ala Ala Ala	
GCC AAG GCC TTC AAG CAC CCA AGC ATC CGC AAT CCT GTC AGC TTG GTG	1200
Ala Lys Ala Phe Lys His Pro Ser Ile Arg Asn Pro Val Ser Leu Val	
GTG ACT CGG CTA GTG ATC CTG GGG TCA GGC GAG GAG GGG CCC CAA GTG	1248
Val Thr Arg Leu Val Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val	
GGG CCC AGT GCT GCC CAG ACC CTG CGC AGC TTC TGT GCC TGG CAG CGG	1296
Gly Pro Ser Ala Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg	
GGC CTC AAC ACC CCT GAG GAC TCG GAC CCT GAC CAC TTT GAC ACA GCC	1344
Gly Leu Asn Thr Pro Glu Asp Ser Asp Pro Asp His Phe Asp Thr Ala	
ATT CTG TTT ACC CGT CAG GAC CTG TGT GGA GTC TCC ACT TGC GAC ACG	1392
Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr	
CTG GGT ATG GCT GAT GTG GGC ACC GTC TGT GAC CCG GCT CGG AGC TGT	1440
Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys	
GCC ATT GTG GAG GAT GAT GGG CTC CAG TCA GCC TTC ACT GCT GCT CAT	1488
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala His	
GAA CTG GGT CAT GTC TTC AAC ATG CTC CAT GAC AAC TCC AAG CCA TGC	1536
Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys Pro Cys	
ATC AGT TTG AAT GGG CCT TTG AGC ACC TCT CGC CAT GTC ATG GCC CCT	1584
Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val Met Ala Pro	
GTG ATG GCT CAT GTG GAT CCT GAG GAG CCC TGG TCC CCC TGC AGT GCC	1632
Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser Pro Cys Ser Ala	
CGC TTC ATC ACT GAC TTC CTG GAC AAT GGC TAT GGG CAC TGT CTC TTA	1680
Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr Gly His Cys Leu Leu	
GAC AAA CCA GAG GCT CCA TTG CAT CTG CCT GTG ACT TTC CCT GGC AAG	1728
Asp Lys Pro Glu Ala Pro Leu His Leu Pro Val Thr Phe Pro Gly Lys	
GAC TAT GAT GCT GAC CGC CAG TGC CAG CTG ACC TTC GGG CCC GAC TCA	1776
Asp Tyr Asp Ala Asp Arg Gln Cys Gln Leu Thr Phe Gly Pro Asp Ser	
CGC CAT TGT CCA CAG CTG CCG CCG CCC TGT GCT GCC CTC TGG TGC TCT	1824
Arg His Cys Pro Gln Leu Pro Pro Pro Cys Ala Ala Leu Trp Cys Ser	

GGC CAC CTC AAT GGC CAT GCC ATG TGC CAG ACC AAA CAC TCG CCC TGG	1872
Gly His Leu Asn Gly His Ala Met Cys Gln Thr Lys His Ser Pro Trp	
GCC GAT GGC ACA CCC TGC GGG CCC GCA CAG GCC TGC ATG GGT GGT CGC	1920
Ala Asp Gly Thr Pro Cys Gly Pro Ala Gln Ala Cys Met Gly Gly Arg	
TGC CTC CAC ATG GAC CAG CTC CAG GAC TTC AAT ATT CCA CAG GCT GGT	1968
Cys Leu His Met Asp Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly	
GGC TGG GGT CCT TGG GGA CCA TGG GGT GAC TGC TCT CGG ACC TGT GGG	2016
Gly Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly	
GGT GGT GTC CAG TTC TCC TCC CGA GAC TGC ACG AGG CCT GTC CCC CGG	2064
Gly Gly Val Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg	
AAT GGT GGC AAG TAC TGT GAG GGC CGC CGT ACC CGC TTC CGC TCC TGC	2112
Asn Gly Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys	
AAC ACT GAG GAC TGC CCA ACT GGC TCA GCC CTG ACC TTC CGC GAG GAG	2160
Asn Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	
CAG TGT GCT GCC TAC AAC CAC CGC ACC GAC CTC TTC AAG AGC TTC CCA	2208
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe Pro	
GGG CCC ATG GAC TGG GTT CCT CGC TAC ACA GGC GTG GCC CCC CAG GAC	2256
Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro Gln Asp	
CAG TGC AAA CTC ACC TGC CAG GCC CGG GCA CTG GGC TAC TAC TAT GTG	2304
Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr Tyr Val	
CTG GAG CCA CGG GTG GTA GAT GGG ACC CCC TGT TCC CCG GAC AGC TCC	2352
Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Ser	
TCG GTC TGT GTC CAG GGC CGA TGC ATC CAT GCT GGC TGT GAT CGC ATC	2400
Ser Val Cys Val Gln Gly Arg Cys Ile His Ala Gly Cys Asp Arg Ile	
ATT GGC TCC AAG AAG AAG TTT GAC AAG TGC ATG GTG TGC GGA GGG GAC	2448
Ile Gly Ser Lys Lys Phe Asp Lys Cys Met Val Cys Gly Gly Asp	
GGT TCT GGT TGC AGC AAG CAG TCA GGC TCC TTC AGG AAA TTC AGG TAC	2496
Gly Ser Gly Cys Ser Lys Gln Ser Gly Ser Phe Arg Lys Phe Arg Tyr	
GGA TAC AAC AAT GTG GTC ACT ATC CCC GCG GGG GCC ACC CAC ATT CTT	2544
Gly Tyr Asn Asn Val Val Thr Ile Pro Ala Gly Ala Thr His Ile Leu	
GTC CGG CAG CAG GGA AAC CCT GGC CAC CGG AGC ATC TAC TTG GCC CTG	2592
Val Arg Gln Gln Gly Asn Pro Gly His Arg Ser Ile Tyr Leu Ala Leu	
AAG CTG CCA GAT GGC TCC TAT GCC CTC AAT GGT GAA TAC ACG CTG ATG	2640
Lys Leu Pro Asp Gly Ser Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met	
CCC TCC CCC ACA GAT GTG GTA CTG CCT GGG GCA GTC AGC TTG CGC TAC	2688
Pro Ser Pro Thr Asp Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr	
AGC GGG GCC ACT GCA GCC TCA GAG ACA CTG TCA GGC CAT GGG CCA CTG	2736
Ser Gly Ala Thr Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu	
GCC CAG CCT TTG ACA CTG CAA GTC CTA GTG GCT GGC AAC CCC CAG GAC	2784
Ala Gln Pro Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp	
ACA CGC CTC CGA TAC AGC TTC TTC GTG CCC CGG CCG ACC CCT TCA ACG	2832
Thr Arg Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr	
CCA CGC CCC ACT CCC CAG GAC TGG CTG CAC CGA AGA GCA CAG ATT CTG	2880

Pro Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu
 GAG ATC CTT CGG CGG CGC CCC TGG GCG GGC AGG AAA TAA CCT CAC TAT 2928
 Glu Ile Leu Arg Arg Pro Trp Ala Gly Arg Lys End

CCC GGC TGC CCT TTC TGG GCA CCG GGG CCT CGG ACT TAG CTG GGA GAA 2976
 AGA GAG AGC TTC TGT TGC TGC CTC ATG CTA AGA CTC AGT GGG GAG GGG 3024
 CTG TGG GCG TGA GAC CTG CCC CTC CTC TCT GCC CTA ATG CGC AGG CTG 3072
 GCC CTG CCC TGG TTT CCT GCC CTG GGA GGC AGT GAT GGG TTA GTG GAT 3120
 GGA AGG GGC TGA CAG ACA GCC CTC CAT CTA AAC TGC CCC CTC TGC CCT 3168
 GCG GGT CAC AGG AGG GAG GGG GAA GGC AGG GAG GGC CTG GGC CCC AGT 3216
 TGT ATT TAT TTA GTA TTT ATT CAC TTT TAT TTA GCA CCA GGG AAG GGG 3264
 ACA AGG ACT AGG GTC CTG GGG AAC CTG ACC CCT GAC CCC TCA TAG CCC 3312
 TCA CCC TGG GGC TAG GAA ATC CAG GGT GGT GAT AGG TAT AAG TGG 3360
 TGT GTG TAT GCG TGT GTG TGT GAA AAT GTG TGT GTG CTT ATG 3408
 TAT GAG GTA CAA CCT GTT CTG CTT TCC TCT TCC TGA ATT TTA TTT TTT 3456
 GGG AAA AGA AAA GTC AAG GGT AGG GTG GGC CTT CAG GGA GTG AGG GAT 3504
 TAT CCT TTT TTT TTT CTT TCT TTC TTT CTT TTT TTT GAG ACA GAA 3552
 TCT CGC TCT GTC GCC CAG GCT GGA GTG CAA TGG CAC AAT CTC GGC TCA 3600
 CTG CAT CCT CCG CCT CCC GGG TTC AAG TGA TTC TCA TGC CTC AGC CTC 3648
 CTG AGT AGC TGG GAT TAC AGG CTC CTG CCA CCA CGC CCG GCT AAT TTT 3696
 TGT TTT GTT TTG TTT GGA GAC AGA GTC TCG CTA TTG TCA CCA GGG CTG 3744
 GAA TGA TTT CAG CTC ACT GCA ACC TTC GCC ACC TGG GTT CCA GCA ATT 3792
 CTC CTG CCT CAG CCT CCC GAG TAG CTG AGA TTA TAG GCA CCT ACC ACC 3840
 ACG CCC GGC TAA TTT TTG TAT TTT TAG TAG AGA CGG GGT TTC ACC ATG 3888
 TTG GCC AGG CTG GTC TCG AAC TCC TGA CCT TAG GTG ATC CAC TCG CCT 3936
 TCA TCT CCC AAA GTG CTG GGA TTA CAG GCG TGA GCC ACC GTG CCT GGC 3984
 CAC GCC CAA CTA ATT TTT GTA TTT TTA GTA GAG ACA GGG TTT CAC CAT 4032
 GTT GGC CAG GCT CTT GAA CTC CTG ACC TCA GGT AAT CGA CCT GCC 4080
 TCG GCC TCC CAA AGT GCT GGG ATT ACA GGT GTG AGC CAC CAC GCC CGG 4128
 TAC ATA TTT TTT AAA TTG AAT TCT ACT ATT TAT GTG ATC CTT TTG GAG 4176
 TCA GAC AGA TGT GGG T 4192

(2) INFORMATION FOR SEQ ID NO:2:
 (i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 837 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg Trp 16
Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro Leu Ser 32
Trp Leu Val Trp Leu Leu Leu Leu Ala Ser Leu Leu Pro Ser 48
Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu Ile Val Phe Pro 64
Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser Gly Ala Pro Ala Arg 80
Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu Thr Leu Leu Leu Glu Leu 96
Glu Gln Asp Ser Gly Val Gln Val Glu Gly Leu Thr Val Gln Tyr Leu 112
Gly Gln Ala Pro Glu Leu Leu Gly Gly Ala Glu Pro Gly Thr Tyr Leu 128
Thr Gly Thr Ile Asn Gly Asp Pro Glu Ser Val Ala Ser Leu His Trp 144
Asp Gly Gly Ala Leu Leu Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu 160
His Leu Gln Pro Leu Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro 176
Gly Ala His Ile Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro 192
Met Cys Asn Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg 208
Arg Ala Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val 224
Val Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg 240
Tyr Leu Leu Thr Val Met Ala Ala Ala Lys Ala Phe Lys His Pro 256
Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val Ile Leu 272
Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala Ala Gln Thr 288
Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn Thr Pro Glu Asp 304
Ser Asp Pro Asp His Phe Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp 320
Leu Cys Gly Val Ser Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly 336
Thr Val Cys Asp Pro Ala Arg Ser Cys Ala Ile Val Glu Asp Asp Gly 352
Leu Gln Ser Ala Phe Thr Ala Ala His Glu Leu Gly His Val Phe Asn 368
Met Leu His Asp Asn Ser Lys Pro Cys Ile Ser Leu Asn Gly Pro Leu 384
Ser Thr Ser Arg His Val Met Ala Pro Val Met Ala His Val Asp Pro 400
Glu Glu Pro Trp Ser Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu 416
Asp Asn Gly Tyr Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu 432
His Leu Pro Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln 448

Cys Gln Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro	464
Pro Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys Gly	496
Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp Gln Leu	512
Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro Trp Gly Pro	528
Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Val Gln Phe Ser Ser	544
Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly Gly Lys Tyr Cys Glu	560
Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn Thr Glu Asp Cys Pro Thr	576
Gly Ser Ala Leu Thr Phe Arg Glu Glu Gln Cys Ala Ala Tyr Asn His	592
Arg Thr Asp Leu Phe Lys Ser Phe Pro Gly Pro Met Asp Trp Val Pro	608
Arg Tyr Thr Gly Val Ala Pro Gln Asp Gln Cys Lys Leu Thr Cys Gln	624
Ala Arg Ala Leu Gly Tyr Tyr Val Leu Glu Pro Arg Val Val Asp	640
Gly Thr Pro Cys Ser Pro Asp Ser Ser Val Cys Val Gln Gly Arg	656
Cys Ile His Ala Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe	672
Asp Lys Cys Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln	688
Ser Gly Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr	704
Ile Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser Tyr	736
Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp Val Val	752
Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr Ala Ala Ser	768
Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro Leu Thr Leu Gln	784
Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg Leu Arg Tyr Ser Phe	800
Phe Val Pro Arg Pro Thr Pro Ser Thr Pro Arg Pro Thr Pro Gln Asp	816
Trp Leu His Arg Arg Ala Gln Ile Leu Glu Ile Leu Arg Arg Arg Pro	832
Trp Ala Gly Arg Lys	837

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

FASLSRVETLVVADDKMAAFHGAGLK

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

YTGVAPR

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ALGYYYVLDPR

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGGGTGGTGTCCAGTTCTCC

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCCCTGGAAAGCTTGAAGAG

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCCGGAATGGTGGCAAGTACTG

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACCCACATCTGTCTGACTCCAAA

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCAGTTGGGCAGTCCTCAGTGTT

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTCGGTGCAGGGTTGTAGGC

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CASLSRFVETLVVADDK

ADMP-2 Sequences

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 3250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 121..2913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGA CTC AAT CCT GCA AGC AAG TGT GTG TGT GTC CCC ATC CCC CGC CCC 48
GTT AAC TTC ATA GCA AAT AAC AAA TAC CCA TAA AGT CCC AGT CGC GCA 96
GCC CCT CCC CGC GGG CAG CGC ACT ATG CTG CTC GGG TGG GCG TCC CTG 144
Met Leu Leu Gly Trp Ala Ser Leu
CTG CTG TGC GCG TTC CGC CTG CCC CTG GCC GCG GTC GGC CCC GCC GCG 192
Leu Leu Cys Ala Phe Arg Leu Pro Ala Ala Val Gly Pro Ala Ala
ACA CCT GCC CAG GAT AAA GCC GGG CAG CCT CCG ACT GCT GCA GCA GCC 240
Thr Pro Ala Gln Asp Lys Ala Gly Gln Pro Pro Thr Ala Ala Ala
GCC CAG CCC CGC CGG CAG GGG GAG GAG GTG CAG GAG CGA GCC GAG 288
Ala Gln Pro Arg Arg Gln Gly Glu Val Gln Glu Arg Ala Glu
CCT CCC GGC CAC CCG CAC CCC CTG GCG CAG CGG CGC AGG AGC AAG GGG 336
Pro Pro Gly His Pro His Pro Leu Ala Gln Arg Arg Ser Lys Gly
CTG GTG CAG AAC ATC GAC CAA CTC TAC TCC GGC GGC AAG GTG GGC 384
Leu Val Gln Asn Ile Asp Gln Leu Tyr Ser Gly Gly Lys Val Gly
TAC CTC GTC TAC GCG GGC CGG AGG TTC CTC TTG GAC CTG GAG CGA 432
Tyr Leu Val Tyr Ala Gly Arg Arg Phe Leu Asp Leu Glu Arg
GAT GGT TCG GTG GGC ATT GCT GGC TTC GTG CCC GCA GGA GGC GGG ACG 480
Asp Gly Ser Val Gly Ile Ala Gly Phe Val Pro Ala Gly Gly Thr
AGT GCG CCC TGG CGC CAC CGG AGC CAC TGC TTC TAT CGG GGC ACA GTG 528
Ser Ala Pro Trp Arg His Arg Ser His Cys Phe Tyr Arg Gly Thr Val
GAC GCT AGT CCC CGC TCT CTG GCT GTC TTT GAC CTC TGT GGG GGT CTC 576
Asp Ala Ser Pro Arg Ser Leu Ala Val Phe Asp Leu Cys Gly Gly Leu
GAC GGC TTC TTC GCG GTC AAG CAC GCG CGC TAC ACC CTA AAG CCA CTG 624
Asp Gly Phe Phe Ala Val Lys His Ala Arg Tyr Thr Leu Lys Pro Leu
CTG CGC GGA CCC TGG GCG GAG GAA GAA AAG GGG CGC GTG TAC GGG GAT 672
Leu Arg Gly Pro Trp Ala Glu Glu Lys Gly Arg Val Tyr Gly Asp
GGG TCC GCA CGG ATC CTG CAC GTC TAC ACC CGC GAG GGC TTC AGC TTC 720
Gly Ser Ala Arg Ile Leu His Val Tyr Arg Glu Gly Phe Ser Phe

GAG GCC CTG CCG CCG CGC GCC AGC TGC GAA ACC CCC GCG TCC ACA CCG 768
Glu Ala Leu Pro Pro Arg Ala Ser Cys Glu Thr Pro Ala Ser Thr Pro

GAG GCC CAC GAG CAT GCT CCG GCG CAC AGC AAC CCG AGC GGA CGC GCA 816
Glu Ala His Glu His Ala Pro Ala His Ser Asn Pro Ser Gly Arg Ala

GCA CTG GCC TCG CAG CTC TTG GAC CAG TCC GCT CTC TCG CCC GCT GGG 864
Ala Leu Ala Ser Gln Leu Leu Asp Gln Ser Ala Leu Ser Pro Ala Gly

GGC TCA GGA CCG CAG ACG TGG TGG CGG CGG CGC CGC TCC ATC TCC 912
Gly Ser Gly Pro Gln Thr Trp Trp Arg Arg Arg Arg Ser Ile Ser

CGG GCC CGC CAG GTG GAG CTG CTT CTG GTG GCT GAC GCG TCC ATG GCG 960
Arg Ala Arg Gln Val Glu Leu Leu Val Ala Asp Ala Ser Met Ala

CGG TTG TAT GGC CGG GGC CTG CAG CAT TAC CTG CTG ACC CTG GCC TCC 1008
Arg Leu Tyr Gly Arg Leu Gln His Tyr Leu Leu Thr Leu Ala Ser

ATC GCC AAT AGG CTG TAC AGC CAT GCT AGC ATC GAG AAC CAC ATC CGC 1056
Ile Ala Asn Arg Leu Tyr Ser His Ala Ser Ile Glu Asn His Ile Arg

CTG GCC GTG GTG AAG GTG GTG CTA GGC GAC AAG GAC AAG AGC CTG 1104
Leu Ala Val Val Lys Val Val Leu Gly Asp Lys Asp Lys Ser Leu

GAA GTG AGC AAG AAC GCT GCC ACC ACA CTC AAG AAC TTT TGC AAG TGG 1152
Glu Val Ser Lys Asn Ala Ala Thr Thr Leu Lys Asn Phe Cys Lys Trp

CAG CAC CAA CAC AAC CAG CTG GGA GAT GAC CAT GAG GAG CAC TAC GAT 1200
Gln His Gln His Asn Gln Leu Gly Asp Asp His Glu Glu His Tyr Asp

GCA GCT ATC CTG TTT ACT CGG GAG GAT TTA TGT GGG CAT CAT TCA TGT 1248
Ala Ala Ile Leu Phe Thr Arg Glu Asp Leu Cys Gly His His Ser Cys

GAC ACC CTG GGA ATG GCA GAC GTT GGG ACC ATA TGT TCT CCA GAG CGC 1296
Asp Thr Leu Gly Met Ala Asp Val Gly Thr Ile Cys Ser Pro Glu Arg

AGC TGT GCT GTG ATT GAA GAC GAT GGC CTC CAC GCA GCC TTC ACT GTG 1344
Ser Cys Ala Val Ile Glu Asp Asp Gly Leu His Ala Ala Phe Thr Val

GCT CAC GAA ATC GGA CAT TTA CTT GGC CTC TCC CAT GAC GAT TCC AAA 1392
Ala His Glu Ile Gly His Leu Leu Gly Leu Ser His Asp Asp Ser Lys

TTC TGT GAA GAG ACC TTT GGT TCC ACA GAA GAT AAG CGC TTA ATG TCT 1440
Phe Cys Glu Glu Thr Phe Gly Ser Thr Glu Asp Lys Arg Leu Met Ser

TCC ATC CTT ACC AGC ATT GAT GCA TCT AAG CCC TGG TCC AAA TGC ACT 1488
Ser Ile Leu Thr Ser Ile Asp Ala Ser Lys Pro Trp Ser Lys Cys Thr

TCA GCC ACC ATC ACA GAA TTC CTG GAT GAT GGC CAT GGT AAC TGT TTG 1536
Ser Ala Thr Ile Thr Glu Phe Leu Asp Asp Gly His Gly Asn Cys Leu

CTG GAC CTA CCA CGA AAG CAG ATC CTG GGC CCC GAA GAA CTC CCA GGA 1584
Leu Asp Leu Pro Arg Lys Gln Ile Leu Gly Pro Glu Glu Leu Pro Gly

CAG ACC TAC GAT GCC ACC CAG CAG TGC AAC CTG ACA TTC GGG CCT GAG 1632
Gln Thr Tyr Asp Ala Thr Gln Gln Cys Asn Leu Thr Phe Gly Pro Glu

TAC TCC GTG TGT CCC GGC ATG GAT GTC TGT GCT CGC CTG TGG TGT GCT 1680
Tyr Ser Val Cys Pro Gly Met Asp Val Cys Ala Arg Leu Trp Cys Ala

GTG GTA CGC CAG GGC CAG ATG GTC TGT CTG ACC AAG AAG CTG CCT GCG 1728
Val Val Arg Gln Gly Gln Met Val Cys Leu Thr Lys Lys Leu Pro Ala

GTG GAA GGG ACG CCT TGT GGA AAG GGG AGA ATC TGC CTG CAG GGC AAA 1776
Val Glu Gly Thr Pro Cys Gly Lys Arg Ile Cys Leu Gln Gly Lys

TGT GTG GAC AAA ACC AAG AAA AAA TAT TAT TCA ACG TCA AGC CAT GGC 1824
Cys Val Asp Lys Thr Lys Lys Tyr Tyr Ser Thr Ser Ser His Gly

AAC TGG GGA TCT TGG GGA TCC TGG GGC CAG TGT TCT CGC TCA TGT GGA 1872
Asn Trp Gly Ser Trp Gly Gln Cys Ser Arg Ser Cys Gly

GGA GGA GTG CAG TTT GCC TAT CGT CAC TGT AAT AAC CCT GCT CCC AGA 1920
Gly Gly Val Gln Phe Ala Tyr Arg His Cys Asn Asn Pro Ala Pro Arg

AAC AAC GGA CGC TAC TGC ACA GGG AAG AGG GCC ATC TAC CGC TCC TG 1968C
Asn Asn Gly Arg Tyr Cys Thr Gly Lys Arg Ala Ile Tyr Arg Ser Cys

AGT CTC ATG CCC TGC CCA CCC AAT GGT AAA TCA TTT CGT CAT GAA CAG 2016
Ser Leu Met Pro Pro Asn Gly Lys Ser Phe Arg His Glu Gln

TGT GAG GCC AAA AAT GGC TAT CAG TCT GAT GCA AAA GGA GTC AAA ACT 2064
Cys Glu Ala Lys Asn Gly Tyr Gln Ser Asp Ala Lys Gly Val Lys Thr

TTT GTG GAA TGG GTT CCC AAA TAT GCA GGT GTC CTG CCA GCG GAT GTG 2112
Phe Val Glu Trp Val Pro Lys Tyr Ala Gly Val Leu Pro Ala Asp Val

TGC AAG CTG ACC TGC AGA GCC AAG GGC ACT GGC TAC TAT GTG GTA TTT 2160
Cys Lys Leu Thr Cys Arg Ala Lys Gly Thr Gly Tyr Val Val Phe

TCT CCA AAG GTG ACC GAT GGC ACT GAA TGT AGG CCG TAC AGT AAT TCC 2208
Ser Pro Lys Val Thr Asp Gly Thr Glu Cys Arg Pro Tyr Ser Asn Ser

GTC TGC GTC CGG GGG AAG TGT GTG AGA ACT GGC TGT GAC GGC ATC ATT 2209
Val Cys Val Arg Gly Lys Cys Val Arg Thr Gly Cys Asp Gly Ile Ile

GGC TCA AAG CTG CAG TAT GAC AAG TGC GGA GTA TGT GGA GGA GAC AAC 2304
Gly Ser Lys Leu Gln Tyr Asp Lys Cys Gly Val Cys Gly Gly Asp Asn

TCC AGC TGT ACA AAG ATT GTT GGA ACC TTT AAT AAG AAA AGT AAG GGT 2352
Ser Ser Cys Thr Lys Ile Val Gly Thr Phe Asn Lys Ser Lys Gly

TAC ACT GAC GTG GTG AGG ATT CCT GAA GGG GCA ACC CAC ATA AAA GTT 2400
Tyr Thr Asp Val Val Arg Ile Pro Glu Gly Ala Thr His Ile Lys Val

CGA CAG TTC AAA GCC AAA GAC CAG ACT AGA TTC ACT GCC TAT TTA GCC 2448
Arg Gln Phe Lys Ala Lys Asp Gln Thr Arg Phe Thr Ala Tyr Leu Ala

CTG AAA AAG AAA AAC GGT GAG TAC CTT ATC AAT GGA AAG TAC ATG ATC 2496
Leu Lys Lys Asn Gly Glu Tyr Leu Ile Asn Gly Lys Tyr Met Ile

TCC ACT TCA GAG ACT ATC ATT GAC ATC AAT GGA ACA GTC ATG AAC TAT 2544
Ser Thr Ser Glu Thr Ile Ile Asp Ile Asn Gly Thr Val Met Asn Tyr

AGC GGT TGG AGC CAC AGG GAT GAC TTC CTG CAT GGC ATG GGC TAC TCT 2592
Ser Gly Trp Ser His Arg Asp Asp Phe Leu His Gly Met Gly Tyr Ser

GCC ACG AAG GAA ATT CTA ATA GTG CAG ATT CTT GCA ACA GAC CCC ACT 2640
Ala Thr Lys Glu Ile Leu Ile Val Gln Ile Leu Ala Thr Asp Pro Thr

AAA CCA TTA GAT GTC CGT TAT AGC TTT TTT GTT CCC AAG AAG TCC ACT 2688
Lys Pro Leu Asp Val Arg Tyr Ser Phe Phe Val Pro Lys Lys Ser Thr

CCA AAA GTA AAC TCT GTC ACT AGT CAT GGC AGC AAT AAA GTG GGA TCA 2736
Pro Lys Val Asn Ser Val Thr Ser His Gly Ser Asn Lys Val Gly Ser

CAC ACT TCG CAG CCG CAG TGG GTC ACG GGC CCA TGG CTC GCC TGC TCT 2784

His Thr Ser Gln Pro Gln Trp Val Thr Gly Pro Trp Leu Ala Cys Ser
 AGG ACC TGT GAC ACA GGT TGG CAC ACC AGA ACG GTG CAG TGC CAG GAT 2832
 Arg Thr Cys Asp Thr Gly Trp His Thr Arg Thr Val Gln Cys Gln Asp
 GGA AAC CGG AAG TTA GCA AAA GGA TGT CCT CTC TCC CAA AGG CCT TCT 2880
 Gly Asn Arg Lys Leu Ala Lys Gly Cys Pro Leu Ser Gln Arg Pro Ser
 GCG TTT AAG CAA TGC TTG TTG AAG AAA TGT TAG CCT GTG GTT ATG ATC 2928
 Ala Phe Lys Gln Cys Leu Leu Lys Lys Cys
 TTA TGC ACA AAG ATA ACT GGA GGA TTC AGC ACC GAT GCA GTC GTG GTG 2976
 AAC AGG AGG TCT ACC TAA CGC ACA GAA AGT CAT GCT TCA GTG ACA TTG 3024
 TCA ACA GGA GTC CAA TTA TGG GCA GAA TCT GCT CTC TGT GAC CAA AAG 3072
 AGG ATG TGC ACT GCT TCA CGT GAC AGT GGT GAC CTT GCA ATA TAG AAA 3120
 AAC TTG GGA GTT ATT GAA CAT CCC CTG GGA TTA CAA GAA ACA CTG ATG 3168
 AAT GTT AAA TCA GGG GAC ATT TGA AGA TGG CAG AAC TGT CTC CCC CTT 3216
 GTC ACC TAC CTC TGA ATA GAA TGT CTT TAA TGG T 3250

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 930 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Leu Gly Trp Ala Ser Leu Leu Leu Cys Ala Phe Arg Leu Pro 16
 Leu Ala Ala Val Gly Pro Ala Ala Thr Pro Ala Gln Asp Lys Ala Gly 32
 Gln Pro Pro Thr Ala Ala Ala Ala Gln Pro Arg Arg Arg Gln Gly 48
 Glu Glu Val Gln Glu Arg Ala Glu Pro Pro Gly His Pro His Pro Leu 64
 Ala Gln Arg Arg Arg Ser Lys Gly Leu Val Gln Asn Ile Asp Gln Leu 80
 Tyr Ser Gly Gly Lys Val Gly Tyr Leu Val Tyr Ala Gly Gly Arg 96
 Arg Phe Leu Leu Asp Leu Glu Arg Asp Gly Ser Val Gly Ile Ala Gly 112
 Phe Val Pro Ala Gly Gly Thr Ser Ala Pro Trp Arg His Arg Ser 128
 His Cys Phe Tyr Arg Gly Thr Val Asp Ala Ser Pro Arg Ser Leu Ala 144
 Val Phe Asp Leu Cys Gly Gly Leu Asp Gly Phe Phe Ala Val Lys His 160
 Ala Arg Tyr Thr Leu Lys Pro Leu Leu Arg Gly Pro Trp Ala Glu Glu 176
 Glu Lys Gly Arg Val Tyr Gly Asp Gly Ser Ala Arg Ile Leu His Val 192
 Tyr Thr Arg Glu Gly Phe Ser Phe Glu Ala Leu Pro Pro Arg Ala Ser 208
 Cys Glu Thr Pro Ala Ser Thr Pro Glu Ala His Glu His Ala Pro Ala 224

His Ser Asn Pro Ser Gly Arg Ala Ala Leu Ala Ser Gln Leu Leu Asp 240
Gln Ser Ala Leu Ser Pro Ala Gly Gly Ser Gly Pro Gln Thr Trp Trp 256
Arg Arg Arg Arg Arg Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu 272
Leu Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln 288
His Tyr Leu Leu Thr Leu Ala Ser Ile Ala Asn Arg Leu Tyr Ser His 304
Ala Ser Ile Glu Asn His Ile Arg Leu Ala Val Val Lys Val Val Val 320
Leu Gly Asp Lys Asp Lys Ser Leu Glu Val Ser Lys Asn Ala Ala Thr 336
Thr Leu Lys Asn Phe Cys Lys Trp Gln His Gln His Asn Gln Leu Gly 352
Asp Asp His Glu Glu His Tyr Asp Ala Ala Ile Leu Phe Thr Arg Glu 368
Asp Leu Cys Gly His His Ser Cys Asp Thr Leu Gly Met Ala Asp Val 384
Gly Thr Ile Cys Ser Pro Glu Arg Ser Cys Ala Val Ile Glu Asp Asp 400
Gly Leu His Ala Ala Phe Thr Val Ala His Glu Ile Gly His Leu Leu 416
Gly Leu Ser His Asp Asp Ser Lys Phe Cys Glu Glu Thr Phe Gly Ser 432
Thr Glu Asp Lys Arg Leu Met Ser Ser Ile Leu Thr Ser Ile Asp Ala 448
Ser Lys Pro Trp Ser Lys Cys Thr Ser Ala Thr Ile Thr Glu Phe Leu 464
Asp Asp Gly His Gly Asn Cys Leu Leu Asp Leu Pro Arg Lys Gln Ile 480
Leu Gly Pro Glu Glu Leu Pro Gly Gln Thr Tyr Asp Ala Thr Gln Gln 496
Cys Asn Leu Thr Phe Gly Pro Glu Tyr Ser Val Cys Pro Gly Met Asp 512
Val Cys Ala Arg Leu Trp Cys Ala Val Val Arg Gln Gly Gln Met Val 528
Cys Leu Thr Lys Lys Leu Pro Ala Val Glu Gly Thr Pro Cys Gly Lys 544
Gly Arg Ile Cys Leu Gln Gly Lys Cys Val Asp Lys Thr Lys Lys Lys 560
Tyr Tyr Ser Thr Ser Ser His Gly Asn Trp Gly Ser Trp Gly Ser Trp 576
Gly Gln Cys Ser Arg Ser Cys Gly Gly Val Gln Phe Ala Tyr Arg 592
His Cys Asn Asn Pro Ala Pro Arg Asn Asn Gly Arg Tyr Cys Thr Gly 608
Lys Arg Ala Ile Tyr Arg Ser Cys Ser Leu Met Pro Cys Pro Pro Asn 624
Gly Lys Ser Phe Arg His Glu Gln Cys Glu Ala Lys Asn Gly Tyr Gln 640
Ser Asp Ala Lys Gly Val Lys Thr Phe Val Glu Trp Val Pro Lys Tyr 656
Ala Gly Val Leu Pro Ala Asp Val Cys Lys Leu Thr Cys Arg Ala Lys 672
Gly Thr Gly Tyr Tyr Val Val Phe Ser Pro Lys Val Thr Asp Gly Thr 688
Glu Cys Arg Pro Tyr Ser Asn Ser Val Cys Val Arg Gly Lys Cys Val 704
Arg Thr Gly Cys Asp Gly Ile Ile Gly Ser Lys Leu Gln Tyr Asp Lys 720
Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys Thr Lys Ile Val Gly 736

Thr	Phe	Asn	Lys	Lys	Ser	Lys	Gly	Tyr	Thr	Asp	Val	Val	Arg	Ile	Pro	752
Glu	Gly	Ala	Thr	His	Ile	Lys	Val	Arg	Gln	Phe	Lys	Ala	Lys	Asp	Gln	768
Thr	Arg	Phe	Thr	Ala	Tyr	Leu	Ala	Leu	Lys	Lys	Asn	Gly	Glu	Tyr	784	
Leu	Ile	Asn	Gly	Lys	Tyr	Met	Ile	Ser	Thr	Ser	Glu	Thr	Ile	Ile	Asp	800
Ile	Asn	Gly	Thr	Val	Met	Asn	Tyr	Ser	Gly	Trp	Ser	His	Arg	Asp	Asp	816
Phe	Leu	His	Gly	Met	Gly	Tyr	Ser	Ala	Thr	Lys	Glu	Ile	Leu	Ile	Val	832
Gln	Ile	Leu	Ala	Thr	Asp	Pro	Thr	Lys	Pro	Leu	Asp	Val	Arg	Tyr	Ser	848
Phe	Phe	Val	Pro	Lys	Lys	Ser	Thr	Pro	Lys	Val	Asn	Ser	Val	Thr	Ser	864
His	Gly	Ser	Asn	Lys	Val	Gly	Ser	His	Thr	Ser	Gln	Pro	Gln	Trp	Val	880
Thr	Gly	Pro	Trp	Leu	Ala	Cys	Ser	Arg	Thr	Cys	Asp	Thr	Gly	Trp	His	896
Thr	Arg	Thr	Val	Gln	Cys	Gln	Asp	Gly	Asn	Arg	Lys	Leu	Ala	Lys	Gly	912
Cys	Pro	Leu	Ser	Gln	Arg	Pro	Ser	Ala	Phe	Lys	Gln	Cys	Leu	Leu	Lys	928
Lys	Cys															930

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

SISRARQVELLLVADASMARMYGRGLQHYLLTLASIANKLYF

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGCCACGACCCTCAAGAACTTT

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCATGGAGGCCATCATCTTCAATCA

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGGAGGGATTATGTGGGCATCA

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGCATTTGGACCAGGGCTTAGA

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

SISRARQVELLAhxC-amide